

BEST AVAILABLE COPY

FIGURE 1B

mCRP1	MKPYFCRVFV	FCFLIRLL--	-----TGEIN	GS-----ADHR	MFSFHNGGVQ	39
mCD28	MT-----	----LRLFL	ALNFFSVQVT	ENKILVKQSP	LLVVDSEVS	38
Consensus	M.....RLL..V.	
mCRP1	ISCKYPETV-	-QQLKMRLFR	--EREV-LCE	LTKTKGSGNA	VSIKNPMLCL	34
mCD28	LSCRYSYNLL	AKEFRASLYK	GVNSDVEVCV	GNGNFTYQPQ	FRSNAEFNCD	33
Consensus	.SC.Y.....L..V..C.C.	
mCRP1	YHLSNNSVSF	FLNNPDSSQG	SYFCSLSIF	DPPPFQERNL	SGGYL-HIYE	133
mCD28	GDFDNETVTF	RLWNLHVNHT	DIYFCKIEFM	YPPPYLDNER	SNGTIIHIKE	133
Consensus	...N..V.F	.L.N.....	..YFC.....	.PPP.....	S.G...HI.E	
mCRP1	SQLC---CQL	KL-W-LPVGC	AA-FVVLLF	GCIL-IIWFS	KKKY----GS	172
mCD28	KHLCHTQSSP	KLFWALVVVA	GVLFCYGLLV	TVALCVIWTN	SRRNRLQVT	188
Consensus	..LC.....	KL.W.L.V..	...F...LL.	...L..IW..	
mCRP1	SVH-DPNSEY	MFMAAVNTNK	KSR-LAGVTS			200
mCD28	TMNMTPRRPG	LTRKPYQPYA	PARDFAAYRP			218
ConsensusP.....R..A....	...		

09890729-080301

FIGURE 2A

ATG CAG CTA AAG TGT CCC TGT TTT GTG TCC TTG GGA ACC AGG CAG	45
M Q L K C P C F V S L G T R Q	5 10 15
CCT GTT TGG AAG AAG CTC CAT GTT TCT AGC GGG TTC TTT TCT GGT	90
P V W K K L H V S S G F F S G	20 25 30
CTT GGT CTG TTC TTG CTG CTG TTG AGC AGC CTC TGT GCT GCC TCT	135
L G L F L L L L S S L C A A S	35 40 45
GCA GAG ACT GAA GTC GGT GCA ATG GTG GGC AGC AAT GTG GTG CTC	180
A *E T E V G A M V G S N V V L	50 55 60
AGC TGC ATT GAC CCC CAC AGA CGC CAT TTC AAC TTG AGT GGT CTG	225
S C I D P H R R H F N L S G L	65 70 75
TAT GTC TAT TGG CAA ATC GAA AAC CCA GAA GTT TCG GTG ACT TAC	270
Y V Y W Q I E N P E V S V T Y	80 85 90
TAC CTG CCT TAC AAG TCT CCA GGG ATC AAT GTG GAC AGT TCC TAC	315
Y L P Y K S P G I N V D S S Y	95 100 105
AAG AAC AGG GGC CAT CTG TCC CTG GAC TCC ATG AAG CAG GGT AAC	360
K N R G H L S L D S M K Q G N	110 115 120
TTC TCT CTG TAC CTG AAG AAT GTC ACC CCT CAG GAT ACC CAG GAG	405
F S L Y L K N V T P Q D T Q E	125 130 135
TTC ACA TGC CGG GTA TTT ATG AAT ACA GCC ACA GAG TTA GTC AAG	450
F T C R V F M N T A T E L V K	140 145 150
ATC TTG GAA GAG GTG GTC AGG CTG CGT GTG GCA GCA AAC TTC AGT	495
I L E E V V R L R V A A N F S	155 160 165
ACA CCT GTC ATC AGC ACC TCT GAT AGC TCC AAC CCG GGC CAG GAA	540
T P V I S T S D S S N P G Q E	170 175 180
CGT ACC TAC ACC TGC ATG TCC AAG AAT GGC TAC CCA GAG CCC AAC	585
R T Y T C M S K N G Y P E P N	185 190 195
CTG TAT TGG ATC AAC ACA ACG GAC AAT AGC CTA ATA GAC ACG GCT	630
L Y W I N T T D N S L I D T A	200 205 210
CTG CAG AAT AAC ACT GTC TAC TTG AAC AAG TTG GGC CTG TAT GAT	675
L Q N N T V Y L N K L G L Y D	215 220 225
GTA ATC AGC ACA TTA AGG CTC CCT TGG ACA TCT CGT GGG GAT GTT	720
V I S T L R L P W T S R G D V	230 235 240

09890729-080301

FIGURE 2A (Con't)

CTG	TGC	TGC	GTA	GAG	AAT	GTG	GCT	CTC	CAC	CAG	AAC	ATC	ACT	AGC	755
L	C	C	V	E	N	V	A	L	H	Q	N	I	T	S	
				245					250					255	
ATT	AGC	CAG	GCA	GAA	AGT	TTC	ACT	GGA	AAT	AAC	ACA	AAG	AAC	CCA	810
I	S	Q	A	E	S	F	T	G	N	N	T	K	N	P	
				260					265					270	
CAG	GAA	ACC	CAC	AAT	AAT	GAG	TTA	AAA	GTC	CTT	GTC	CCC	GTC	CTT	855
Q	E	T	H	N	N	E	L	K	V	L	V	P	V	L	
				275					280					285	
GCT	GTA	CTG	GCG	GCA	GCG	GCA	TTC	GTT	TCC	TTC	ATC	ATA	TAC	AGA	900
A	V	L	A	A	A	A	F	V	S	F	I	I	Y	R	
				290					295					300	
CGC	ACG	CGT	CCC	CAC	CGA	AGC	TAT	ACA	GGA	CCC	AAG	ACT	GTA	CAG	945
R	T	R	P	H	R	S	Y	T	G	P	K	T	V	Q	
				305					310					315	
CTT	GAA	CTT	ACA	GAC	CAC	GCC									966
L	E	L	T	D	H	A									
				320		322									

09890729-080304

FIGURE 2B

mB7RP1	MQLKCPCFVS	LGTRQPVWKK	LHVSSGFFSG	LGLFLLLLS-	SLCAASAETE	49
mCD80	MA--CNC--Q	LMQDTPL---	LKFPCPRLI-	L-LFVLLIRL	SQVSSDVDEQ	41
Consensus	M...C.C...	L....P....	L.....	L.LF.LL...	S.....	
mB7RP1	VGAMVGSNVV	LSCIDPHRRH	FNLSGLYVYW	QIENPEVSVT	YYLPYKSPGI	99
mCD80	LSKSVKDKVL	LPC-RYNSPH	EDESEDRIYW	QKHKV---	--LSVIAGKL	35
ConsensusV...V.	L.C.....H	...S....YW	Q.....V...	..L.....	
mB7RP1	NVDSSYKNRG	HLSLDSMKQG	NFSLYLKQVT	PQDTQEFTCR	VFMNTATELV	149
mCD80	KVWPEYKNR-	--TL--YDNT	TYSLIILGLV	LSDRGTYSKV	VQKKEGTYE	130
Consensus	.V...YKNR.	...L.....	..SL.....	..D.....C.	V.....	
mB7RP1	KILEEVVRLR	VAANFSTPVI	STSDSSNPGQ	ERTYTCMSKN	GYPEPNLYWI	199
mCD80	VKHLALVKLS	IKADFSTPNI	TESGNPSADT	KRI-TCFASG	GFPKPRFSWL	179
ConsensusV.L.	...A.FSTP.I	..S.....	.R..TC....	G.P.P...W.	
mB7RP1	-NTTNSLID	TALQNTVYL	NKLGLYDVIS	TLRLPWTSRG	DVLCCVENVA	248
mCD80	ENGRELPGIN	TTISQDPESE	LYTISSQLDF	NTTRNHTIKC	LIKYGDAHVS	229
Consensus	.N.....I.	T.....T...V.	
mB7RP1	LHQNITSISQ	AESFTGNNTK	NPQETHNNEL	KVLVPVLAVL	A-AAAFVSFI	297
mCD80	EDFTWEKPPE	DPPDSKNTLV	LFGAGFGAVI	TVVVIVVIK	CFCKHRSCFR	279
ConsensusN...V.V.V.....F.	
mB7RP1	IYRRTTR-PHR	SYT-GPKTVQ	LELTDHA			322
mCD80	RNEASRETN	SLTFGPPEAL	AEQTVFL			306
Consensus	...R....	S.T.GP...	.E.T...			

09890729-080304

FIGURE 3A

ATG CGG CTG GGC AGT CCT GGA CTG CTC TTC CTG CTC TTC AGC AGC	45
M R L G S P G L L F L L F S S	
5 10 15	
CTT CGA GCT GAT ACT CAG GAG AAG GAA GTC AGA GCG ATG GTA GGC	90
L R A *D *T *Q *E K *E V R A *M V G	
20 25 30	
AGC GAC GTG GAG CTC AGC TGC GCT TGC CCT GAA GGA AGC CGT TTT	135
S D V E L S C A C P E G S R F	
35 40 45	
GAT TTA AAT GAT GTT TAC GTA TAT TGG CAA ACC AGT GAG TCG AAA	180
D L N D V Y V Y W Q T S E S K	
50 55 60	
ACC GTG GTG ACC TAC CAC ATC CCA CAG AAC AGC TCC TTG GAA AAC	225
T V V T Y H I P Q N S S L E N	
65 70 75	
GTG GAC AGC CGC TAC CGG AAC CGA GCC CTG ATG TCA CCG GCC GGC	270
V D S R Y R N R A L M S P A G	
80 85 90	
ATG CTG CGG GGC GAC TTC TCC CTG CGC TTG TTC AAC GTC ACC CCC	315
M L R G D F S L R L F N V T P	
95 100 105	
CAG GAC GAG CAG AAG TTT CAC TGC CTG GTG TTG AGC CAA TCC CTG	360
Q D E Q K F H C L V L S Q S L	
110 115 120	
GGA TTC CAG GAG GTT TTG AGC GTT GAG GTT ACA CTG CAT GTG GCA	405
G F Q E V L S V E V T L H V A	
125 130 135	
GCA AAC TTC AGC GTG CCC GTC GTC AGC GCC CCC CAC AGC CCC TCC	450
A N F S V P V V S A P H S P S	
140 145 150	
CAG GAT GAG CTC ACC TTC ACG TGT ACA TCC ATA AAC GGC TAC CCC	495
Q D E L T F T C T S I N G Y P	
155 160 165	
AGG CCC AAC GTG TAC TGG ATC AAT AAG ACG GAC AAC AGC CTG CTG	540
R P N V Y W I N K T D N S L L	
170 175 180	
GAC CAG GCT CTG CAG AAT GAC ACC GTC TTC TTG AAC ATG CGG GGC	585
D Q A L Q N D T V F L N M R G	
185 190 195	
TTG TAT GAC GTG GTC AGC GTG CTG AGG ATC GCA CGG ACC CCC AGC	630
L Y D V V S V L R I A R T P S	
200 205 210	
GTG AAC ATT GGC TGC TGC ATA GAG AAC GTG CTT CTG CAG CAG AAC	675
V N I G C C I E N V L L Q Q N	
215 220 225	
CTG ACT GTC GGC AGC CAG ACA GGA AAT GAC ATC GGA GAG AGA GAC	720
L T V G S Q T G N D I G E R D	
230 235 240	

09890729-000301

7/33

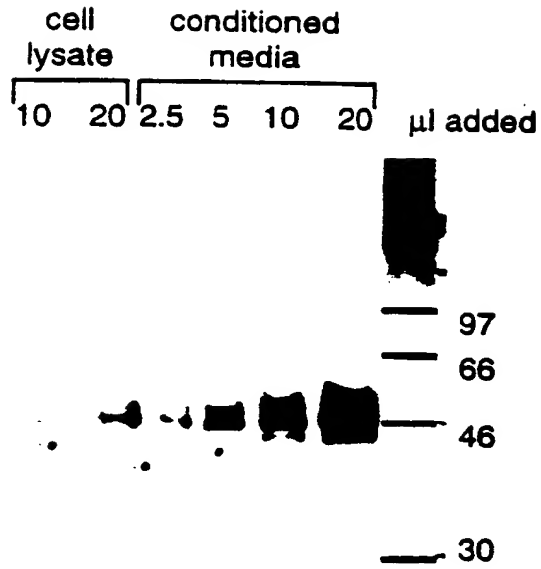
FIGURE 3A (Con't)

AAG ATC ACA GAG AAT CCA GTC AGT ACC GGC GAG AAA AAC GCG GCC	765
K I T E N P V S T G E K N A A	
245 250 255	
ACG TGG AGC ATC CTG GCT GTC CTG TGC CTG CTT GTG GTC GTG GCG	810
T W S I L A V L C L L V V V A	
260 265 270	
GTG GCC ATA GGC TGG GTG TGC AGG GAC CGA TGC CTC CAA CAC AGC	855
V A I G W V C R D R C L Q H S	
275 280 285	
TAT GCA GGT	864
Y A G	
288	

09890729-080304

hB7RP1	EKEVRAMVGS	DVELSCACPE	GSRFDLNDVY	VYWQTSSEKT	VVTYHIPQNS	30
mB7RP1	ETEVGAMVGS	NVVLSCIDPH	RRHFNLSGLY	VYWQIENPEV	SVTTYLPYKS	30
Consensus	E.EV.AMVGS	.V.LSC..P.	#...F.L...Y	VYWQ.....	.VTY...P..S	
hB7RP1	SLENVDSRYR	NRALMSPAGM	LRGDFSLRLF	NVTPQDEQKF	HCLVLSQ-SL	99
mB7RP1	PGINVDSSYK	NRGHLSLDSM	KQGNFSLYLK	NVTPQDTQEF	TCRVFMNTAT	100
Consensus	...NVDS.Y.	NR...S...M	..G.FSL.L.	NVTPQD.Q.F	.C.V.....	
hB7RP1	GFQEVLSVEV	TLHVAANFSV	PVVSAPHSPS	Q-DELTFCT	SINGYPRPNV	143
mB7RP1	ELVKILEEVV	RLRVAANFST	PVISTDSSN	PGQERTYTCM	SKNGYPEPNL	150
ConsensusL...V	.L.VAANFS.	PV.S...S..	...E.T.TC.	S.NGY.P.PN.	
hB7RP1	YWINKTDNSL	LDQALQNDTV	FLNMRGLYDV	VSVLRIARTP	SVNIGCCIEI	198
mB7RP1	YWINTTDNSL	IDTALQNNTV	YLNKGLYDV	ISTLRLPWTS	RGDVLCCVEN	200
Consensus	YWIN.TDNSL	.D.ALQN.TV	.LN..GLYDV	.S.LR...T.CC.EN	
hB7RP1	VLLQQNLTVG	SQTGNDIGER	DKITENPVST	GEKNAATWSI	LAVLCLLVVV	248
mB7RP1	VALHQNITSI	SQAESFTGNN	TKNPQETHNN	ELKVLV--PV	LAVLAAAFV	248
Consensus	V.L.QN.T..	SQ...G..	.K.....K..	..K...7...	LAVL.....V	
hB7RP1	AVAIGWVCRD	RCLQHSYAG				257
mB7RP1	SFIIYR--RT	R-PHRSYTG	KTVQLELTDH	A		276
Consensus	...I...R.	R...SY.G.				

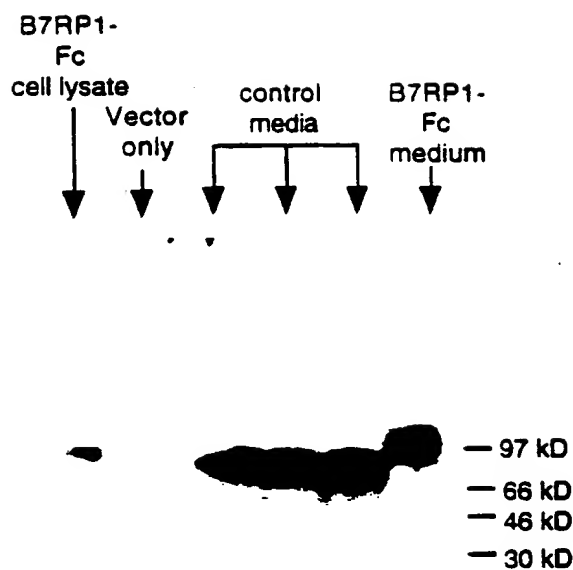
Figure 4A



09890729-080301

10/33

Figure 4B

09890729-08301
T0E080-62/06860

FOE080-62206850

FOE080-62206850

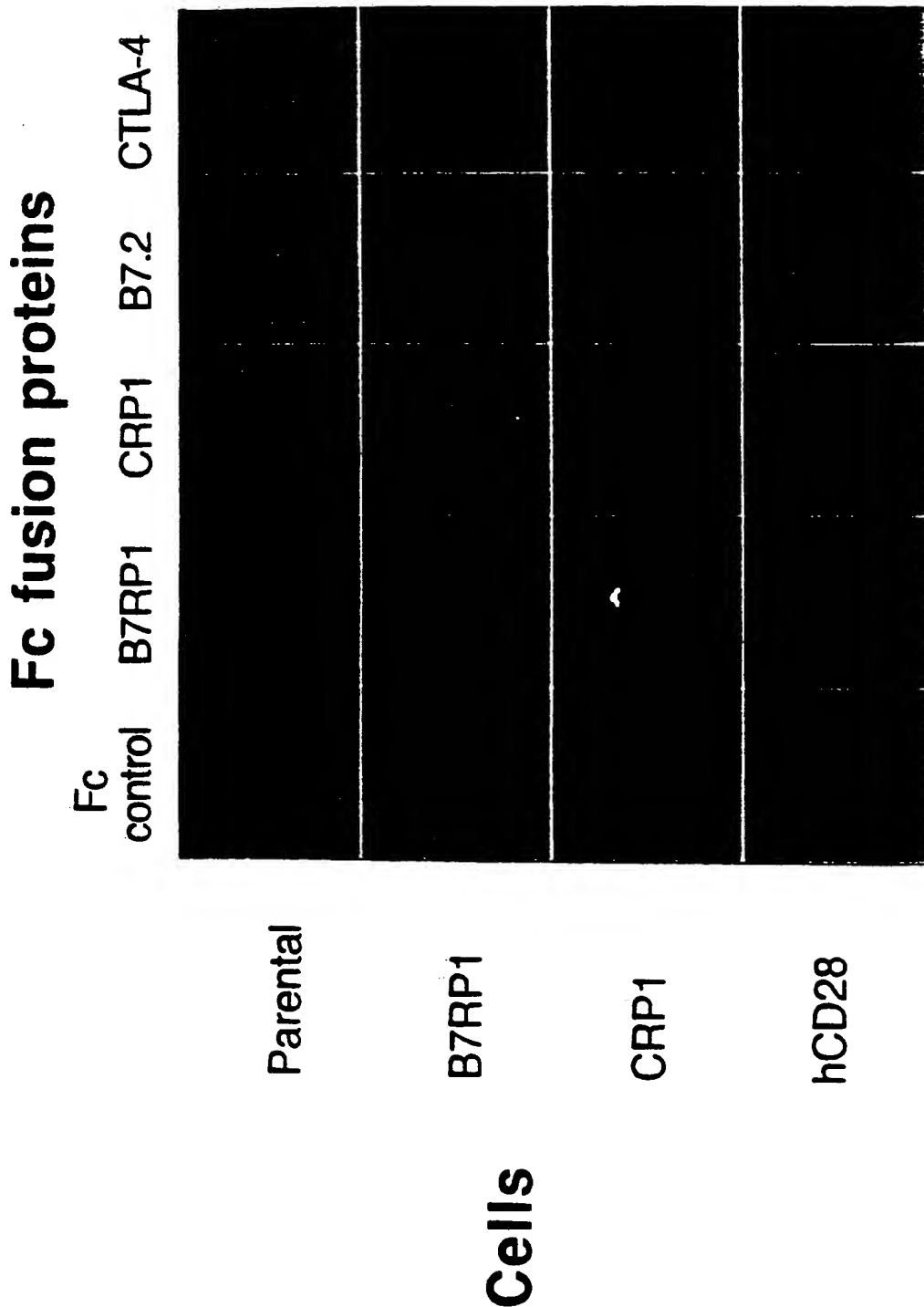
WO 00/46240

11/33

09/890729

PCT/US00/01871

Figure 5



12/33

Figure 6

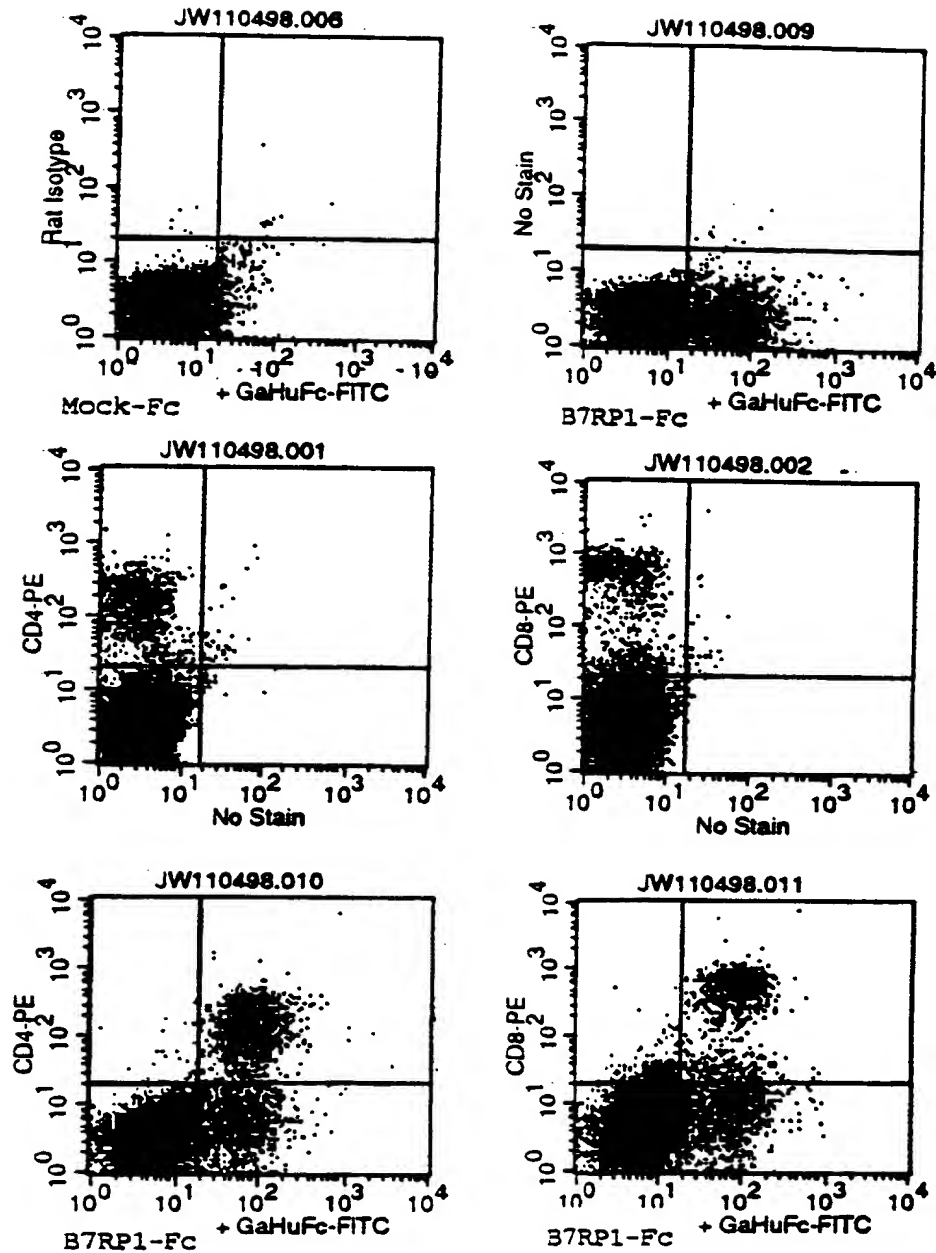
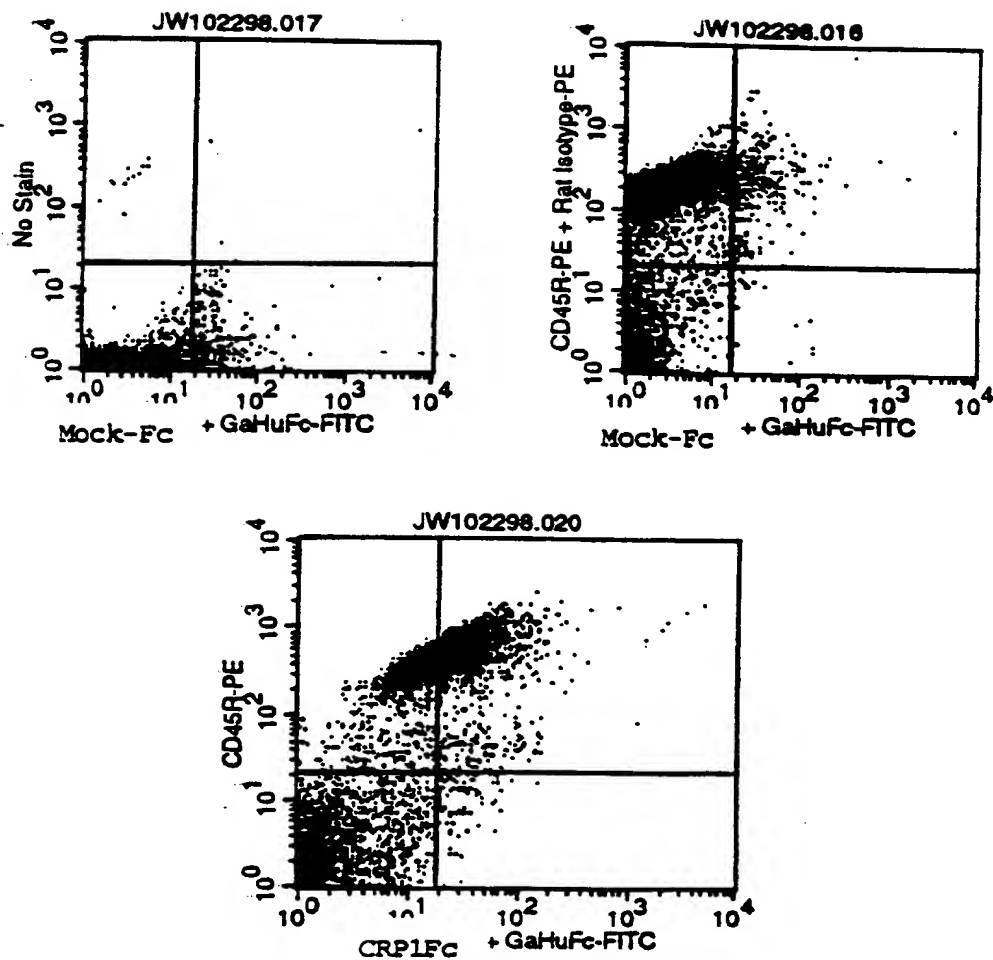
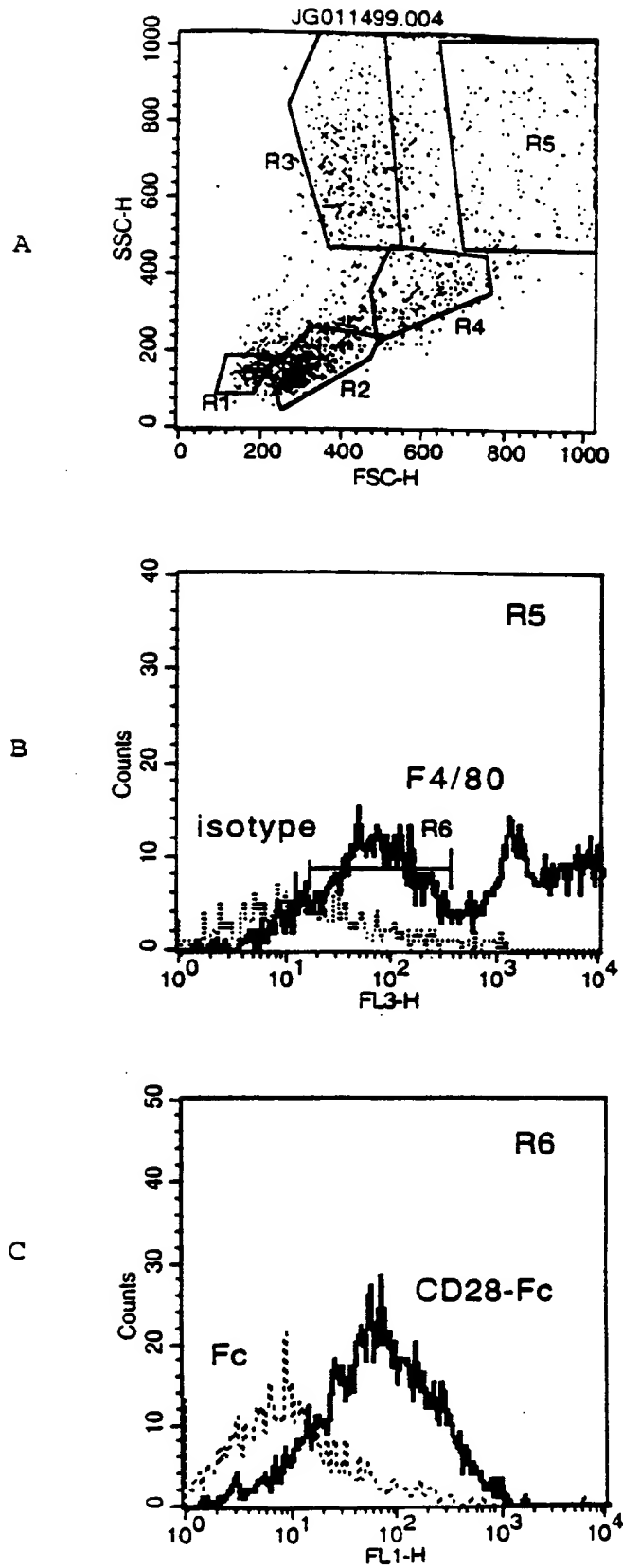


Figure 7



FOI080-62405860

Figure 8



09890729-62206850

FIGURE 9

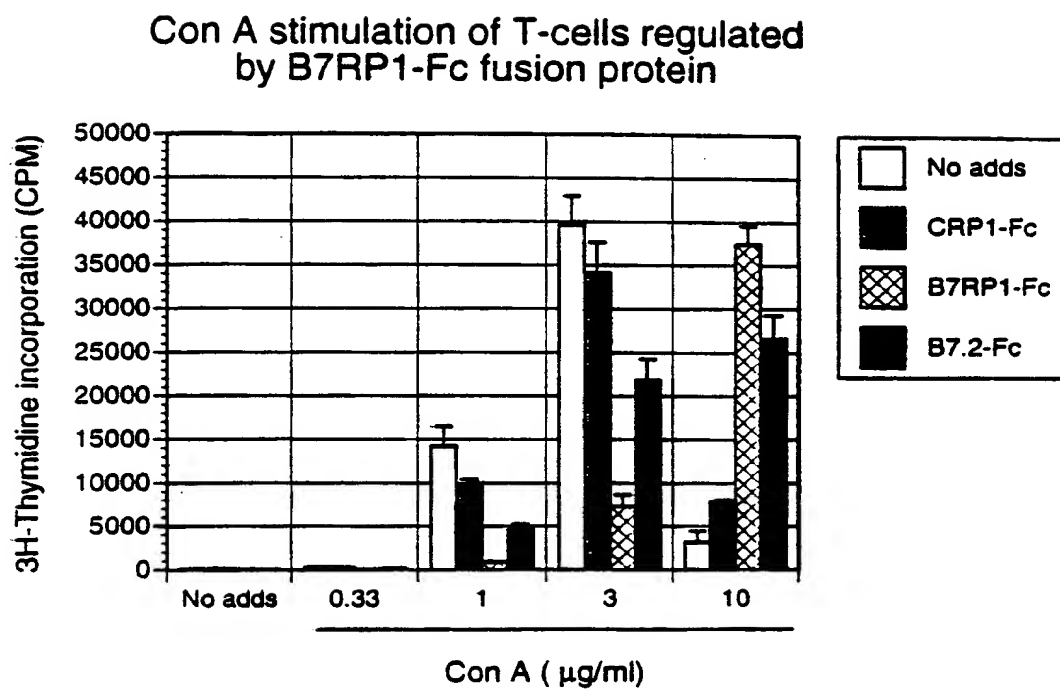


Figure 10

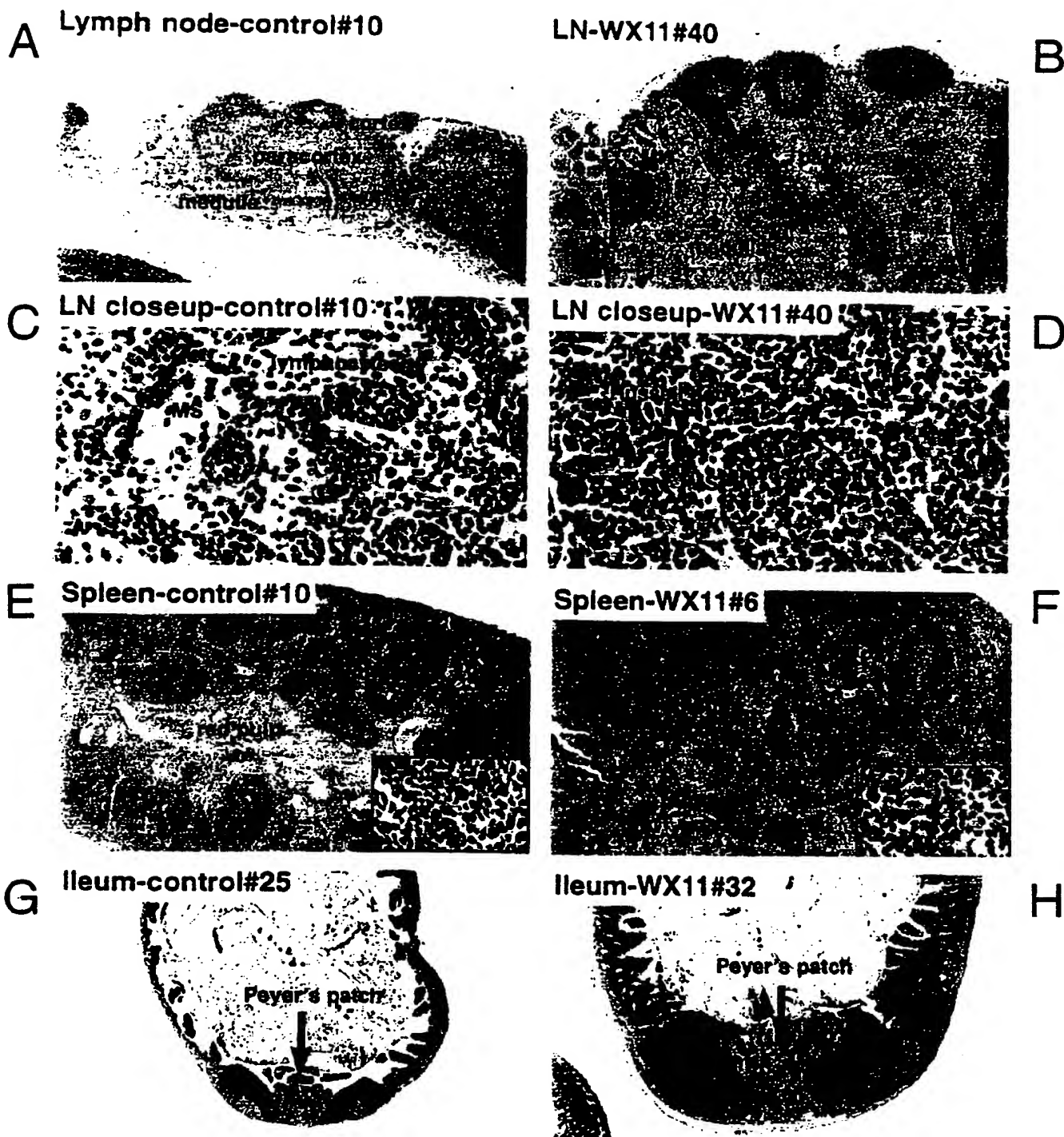
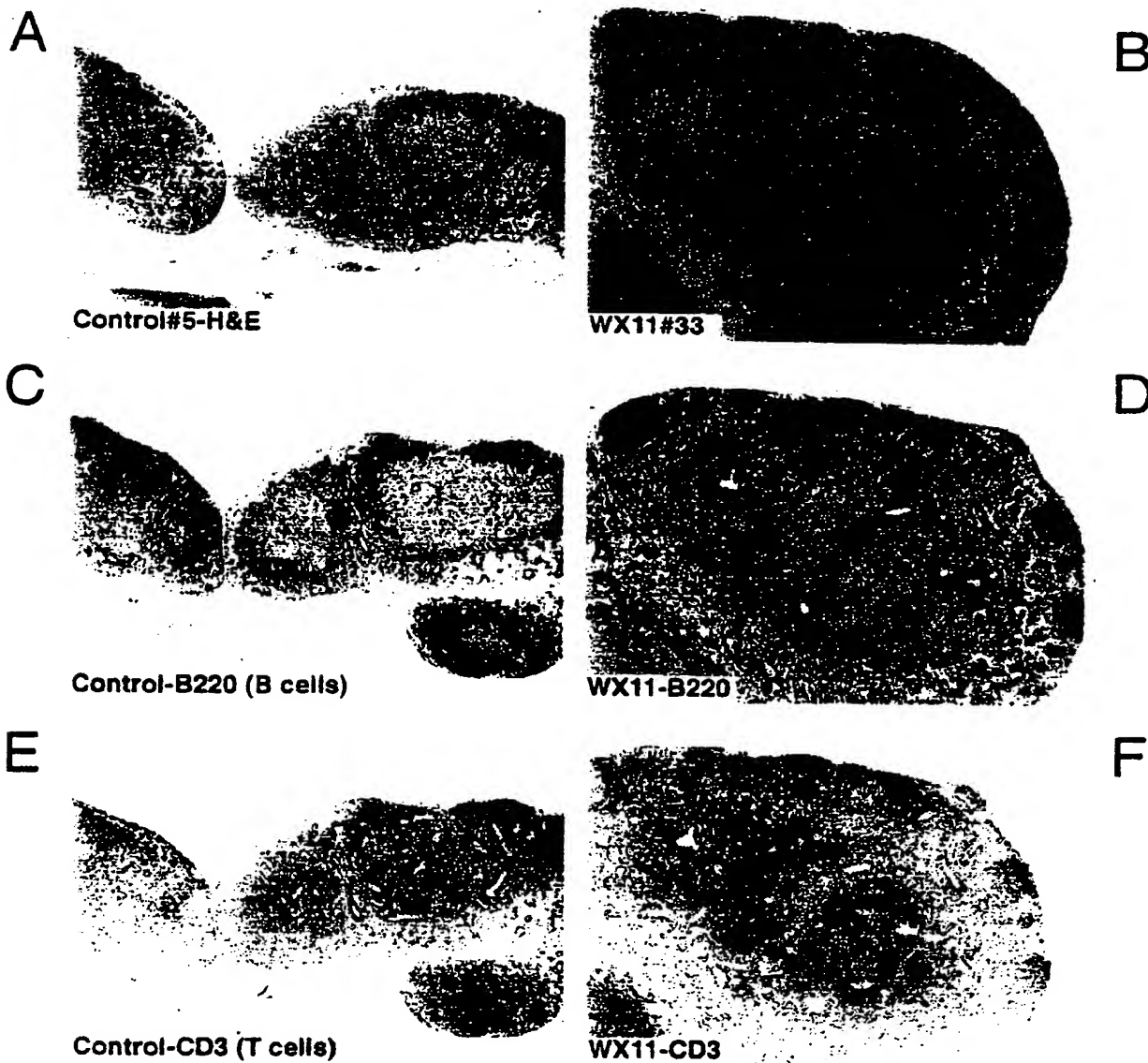


Figure 11



09890729-080301

18/33

Figure 12A.

GCTGGTACGCCTGCAGGTACCGGTCCGGAATTCCCGGGTCCGACCCACGCGTCCGCCCACGCG -138
 TCCGCGGGAGCGCAGTTAGAGCCGATCTCCCGCGCCCCGAGGTTGCTCCTCTCCGAGGTCTC -76
 CCGCGGCCCCAAGTTCTCCGCGCCCCGAGGTCTCCGCGCCCCGAGGTCTCCGCGCCCCGAGGT -14
 CTCCGCCCCGACC -1

ATG CGG CTG GGC AGT CCT GGA CTG CTC TTC CTG CTC TTC AGC AGC 45
 M R L G S P G L L F L L F S S
 5 10 15

CTT CGA GCT GAT ACT CAG GAG AAG GAA GTC AGA GCG ATG GTA GGC 90
 L R A *D *T *Q *E K *E V R A *M V G
 20 25 30

AGC GAC GTG GAG CTC AGC TGC GCT TGC CCT GAA GGA AGC CGT TTT 135
 S D V E L S C A C P E G S R F
 35 40 45

GAT TTA AAT GAT GTT TAC GTA TAT TGG CAA ACC AGT GAG TCG AAA 180
 D L N D V Y V Y W Q T S E S K
 50 55 60

ACC GTG GTG ACC TAC CAC ATC CCA CAG AAC AGC TCC TTG GAA AAC 225
 T V V T Y H I P Q N S S L E N
 65 70 75

GTG GAC AGC CGC TAC CGG AAC CGA GCC CTG ATG TCA CCG GCC GGC 270
 V D S R Y R N R A L M S P A G
 80 85 90

ATG CTG CGG GGC GAC TTC TCC CTG CGC TTG TTC AAC GTC ACC CCC 315
 M L R G D F S L R L F N V T P
 95 100 105

CAG GAC GAG CAG AAG TTT CAC TGC CTG GTG TTG AGC CAA TCC CTG 360
 Q D E Q K F H C L V L S Q S L
 110 115 120

GGA TTC CAG GAG GTT TTG AGC GTT GAG GTT ACA CTG CAT GTG GCA 405
 G F Q E L S V E V T L H V A
 125 130 135

GCA AAC TTC AGC GTG CCC GTC GTC AGC GCC CCC CAC AGC CCC TCC 450
 A N F S V P V V S A P H S P S
 140 145 150

CAG GAT GAG CTC ACC TTC ACG TGT ACA TCC ATA AAC GGC TAC CCC 495
 Q D E L T F T C T S I N G Y P
 155 160 165

AGG CCC AAC GTG TAC TGG ATC AAT AAG ACG GAC AAC AGC CTG CTG 540
 R P N V Y W I N K T D N S L L
 170 175 180

GAC CAG GCT CTG CAG AAT GAC ACC GTC TTC TTG AAC ATG CGG GGC 585
 D Q A L Q N D T V F L N M R G
 185 190 195

TTG TAT GAC GTG GTC AGC GTG CTG AGG ATC GCA CGG ACC CCC AGC 630
 L Y D V V S V L R I A R T P S
 200 205 210

GTG AAC ATT GGC TGC TGC ATA GAG AAC GTG CTT CTG CAG CAG AAC 675
 V N I G C C I E N V L L Q Q N
 215 220 225

09890729-080301

19/33

CTG ACT GTC GGC AGC CAG ACA GGA AAT GAC ATC GGA GAG AGA GAC 720
L T V G S Q T G N D I G E R D
230 235 240

AAG ATC ACA GAG AAT CCA GTC AGT ACC GGC GAG AAA AAC GCG GCC 765
K I T E N P V S T G E K N A A
245 250 255

ACG TGG AGC ATC CTG GCT GTC CTG TGC CTG CTT GTG GTC GTG GCG 810
T W S I L A V L C L L V V V A
260 265 270

GTG GCC ATA GGC TGG GTG TGC AGG GAC CGA TGC CTC CAA CAC AGC 855
V A I G W V C R D R C L Q H S
275 280 285

TAT GCA GGT GCC TGG GCT GTG AGT CCG GAG ACA GAG CTC ACT GGC 900
Y A G A W A V S P E T E L T G
300

CAC GTT TGA 909
H V STOP
302

CCGGAGCTCACC GCCCAGAGCGTGGACAGGGCTTCCGTGAGACGCCACCGTGAGAGGCCAGG 971
TGGCAGCTTGAGCATGGACTCCCAGACTGCAGGGGAGCACTTGGGGCAGCCCCAGAAAGGAC 1033
CACTGCTGGATCCCAGGGAGAACCTGCTGGCGTTGGCTGTGATCCTGGAATGAGGCCCTTTC 1095

09890729-080304

Figure 12B.

human	MRLGSP----	-----G	L-LF-LLFSS	LRADTQEKEV	25
mouse	MQLKPCPCFVS	LGTRQPVWKK	LHVSSGFFSG	LGLFLLLSS	50
Consensus	M.L..P....G	L.LF.LL.SS	L.A...E.EV	50
human	RAMVGSDEL	SCACPEGSRF	DLNDVYVYVQ	TSESKTVVTY	75
mouse	GAMVGSNVVL	SCIDPHRRHF	NLSGLYVYVQ	IENPEVSVTY	100
Consensus	.AMVGS.V.L	SC..P....F	.L...YVYVQVTY	100
human	VDSRYRNRAL	MSPAGMLRGD	FSLRLFNVT	QDEQKFHCLV	124
mouse	VDSSYKNRGH	LSLDSMKQGN	FSLYLKNVT	QDTQEFTCRV	150
Consensus	VDS.Y.NR..	.S...M..G.	FSL.L.NVT	QD.Q.F.C.V	150
human	VLSVEVTLHV	AANFSVPVVS	APHSPSQ-DE	LTFTCTSING	173
mouse	ILEEVVRLRV	AANFSTPVIS	TSDSSNPGQE	RTYTCMSKNG	200
Consensus	.L...V.L.V	AANFS.PV.S	...S.....E	.T.TC.S.NG	200
human	KTDNSLLDQA	LQNDTVFLNM	RGLYDVVSVL	RIARTPSVNI	223
mouse	TTDNSLIDTA	LQNTTVYLNK	LGLYDVISTL	RLPWTSRGDV	250
Consensus	.TDNSL.D.A	LQN.TV.LN.	.GLYDV.S.L	R...T.....	250
human	QNLTVGSQTG	NDIGERDKIT	ENPVSTGEKN	AATWSILAVL	273
mouse	QNITSISQAE	SFTGNNTKNP	QETHNNELKV	LV--PVLAVL	298
Consensus	QN.T..SQ..	...G...K..K.LAVL	300
human	GWVCRDRCLQ	HSYAGAWAVS	PETELTGHV		302
mouse	YR--RTR-PH	RSYTGPKTVQ	LE--LTDHA		322
ConsensusR.R...	.SY.G...V.	.E..LT.H.		329

09890729-00001

Figure 13A

AACAATTTTCACACAGGAAACAGCTATGACCATGATTACGCCAAGCTCTAATACGA -111
CTCACTATAGGGAAAGCTGGTACGCCTGCAGGTACCGGTCCGGAATTCCCGGGTC -56
GACCCACGCGTCCGTGAACACTGAACGCGAGGACTGTTAAGTGTCTTCTGGCAAAC -1

ATG AAG TCA GGC CTC TGG TAT TTC TTT CTC TTC TGC TTG CGC ATT 45
M K S G L W Y F F L F C L R I 15
5 10 15

AAA GTT TTA ACA GGA GAA ATC AAT GGT TCT GCC AAT TAT GAG ATG 90
K V L T *G *E I N G S A N Y E M 30
20 25 30

TTT ATA TTT CAC AAC GGA GGT GTA CAA ATT TTA TGC AAA TAT CCT 135
F I F H N G G V Q I L C K Y P 45
35 40 45

GAC ATT GTC CAG CAA TTT AAA ATG CAG TTG CTG AAA GGG GGG CAA 180
D I V Q Q F K M Q L L K G G Q 60
50 55 60

ATA CTC TGC GAT CTC ACT AAG ACA AAA GGA AGT GGA AAC ACA GTG 225
I L C D L T K T K G S G N T V 75
65 70 75

TCC ATT AAG AGT CTG AAA TTC TGC CAT TCT CAG TTA TCC AAC AAC 270
S I K S L K F C H S Q L S N N 90
80 85 90

AGT GTC TCT TTT TTT CTA TAC AAC TTG GAC CAT TCT CAT GCC AAC 315
S V S F F L Y N L D H S H A N 105
95 100 105

TAT TAC TTC TGC AAC CTA TCA ATT TTT GAT CCT CCT CCT TTT AAA 360
Y Y F C N L S I F D P P P F K 120
110 115 120

GTA ACT CTT ACA GGA GGA TAT TTG CAT ATT TAT GAA TCA CAA CTT 405
V T L T G G Y L H I Y E S Q L 135
125 130 135

TGT TGC CAG CTG AAG TTC TGG TTA CCC ATA GGA TGT GCA GCC TTT 450
C C Q L K F W L P I G C A A F 150
140 145 150

GTT GTA GTC TGC ATT TTG GGA TGC ATA CTT ATT TGT TGG CTT ACA 495
V V V C I L G C I L I C W L T 165
155 160 165

AAA AAG AAG TAT TCA TCC AGT GTG CAC GAC CCT AAC GGT GAA TAC 540
K K K Y S S S V H D P N G E Y 180
170 175 180

ATG TTC ATG AGA GCA GTG AAC ACA GCC AAA AAA TCT AGA CTC ACA 585
M F M R A V N T A K K S R L T 195
185 190 195

GAT GTG ACC CTA TAA 600
D V T L STOP 199

TATGGAAGTCTGGCACCCAGGCATGAAGCACGTTGGCCAGTTTTCTCACTTGA 655
AGTGCAAGATTCTCTTATTTCCGGGACCGGAGAGTCTGACTTAACTACATACA 710

09890729-000001

TCTTCTGCTGGTGTGTTTTGTTCAATCTGGAAGAATGACTGTATCAGTCAATGGGGA	765
TTTTAACAGACTGCCTTGGTACTGCCGAGTCCTCTCAAAACAAACACCCTCTTGC	820
AACCAGCTTTGGAGAAAGCCCAGCTCCTGTGTGCTCACTGGGAGTGGAATCCCTG	875
TCTCCACATCTGCTCCTAGCAGTGCATCAGCCAGTAAAAACAAACACATTTACAAG	930
AAAAATGTTTTAAAGATGCCAGGGGTACTGAATCTGCAAAGCAAATGAGCAGCCA	985
AGGACCAGCATCTGTCCGCATTTCACTATCATACTACCTCTTCTTTCTGTAGGGA	1040
TGAGAATTCCTCTTTTAATCAGTCAAGGGAGATGCTTCAAAGCTGGAGCTATTTT	1095
ATTTCTGAGATGTTGATGTGAAGTGTACATTAGTACATACTCAGTACTCTCCTTC	1150
AATTGCTGAACCCCAGTTGACCATTTTACCAAGACTTTAGATGCTTTCTTGTGCC	1205

09890729-080304

Figure 13B

hCRP1	MKSGLWYFFLFCLRIKVL TGEINGSANYEMFIFHNGGVQILCKYPDIVQQ	50
mCRP1	MKPYFCRVFVFCFLIRLLTGEINGSADHRMFSFHNGGVQISCKYPETVQQ	50
hCRP1	FKMQLLKGGQILCDLT KTKGSGNTVSIKSLKFCHSQLSNNSVSFFLYNLD	100
mCRP1	LKMRLFREREVLCELT KTKGSGNAVSIKNPMLCLYHLSNNSVSFFLNND	100
hCRP1	HSYANYFCNLSIFDPPPFKV.TLTGGYLHIYESQLCCQLKFWLPIGCAA	149
mCRP1	SSQGSYYFCSLSIFDPPPFQERNLSGGYLHIYESQLCCQLKLWLPVGCAA	150
hCRP1	FVVVCILGCILICWLTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTL	199
mCRP1	FVVVLLFGCILIIFWFSKKKYGSSSVHDPNSEYMFMAAVNTNKKSLAGVTS	200

FOE030-62/06860

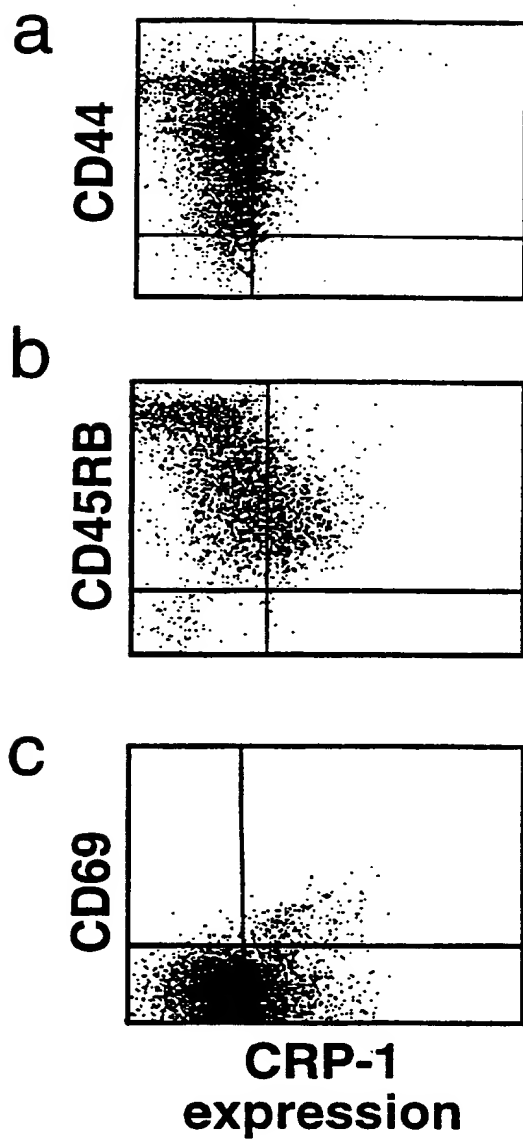


Figure 14

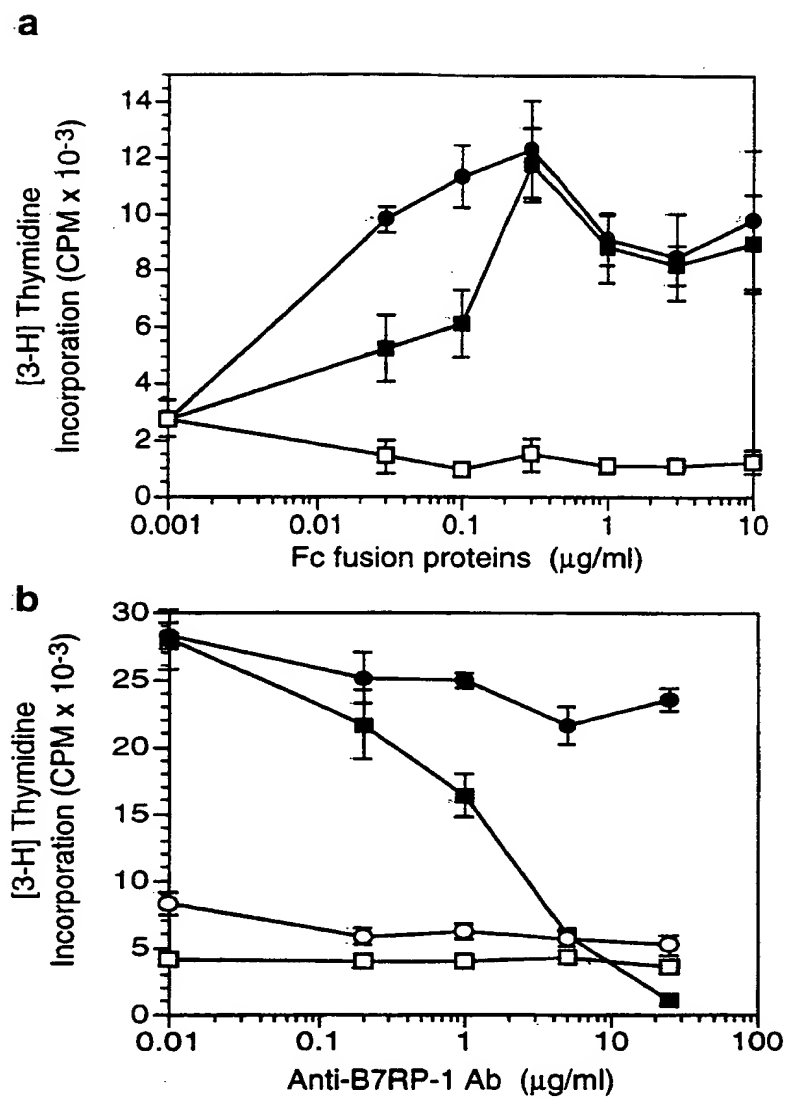
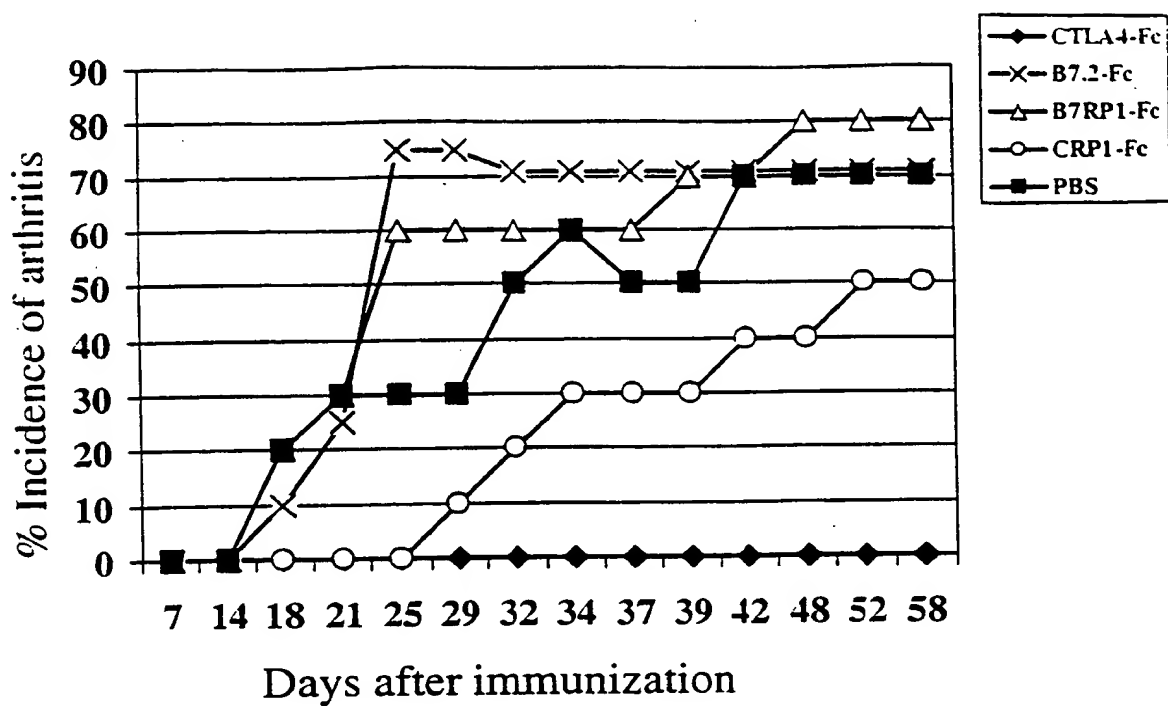


Figure 15

26/33

A.



B.

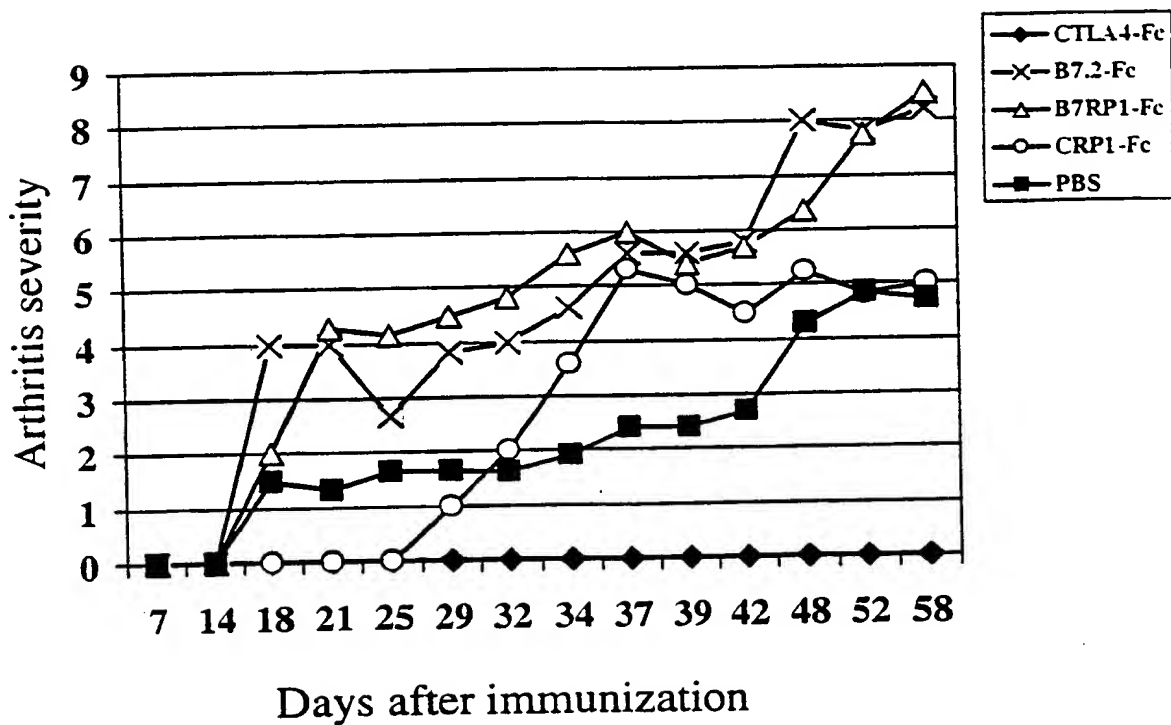


Figure 16

Figure 20

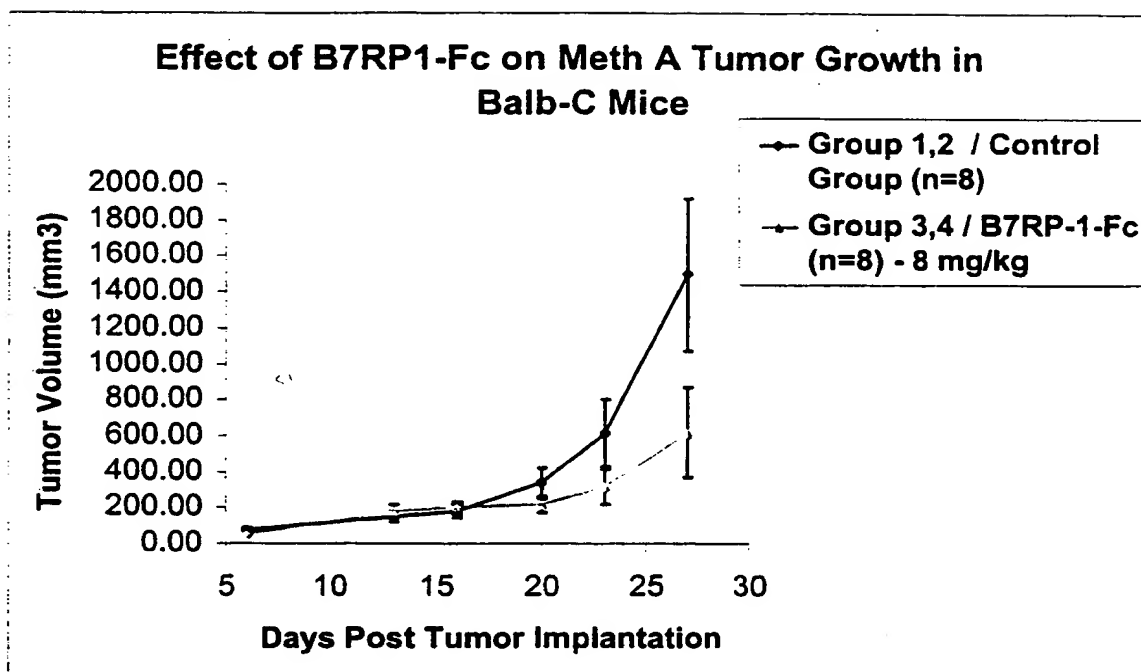


Figure 21A/B.

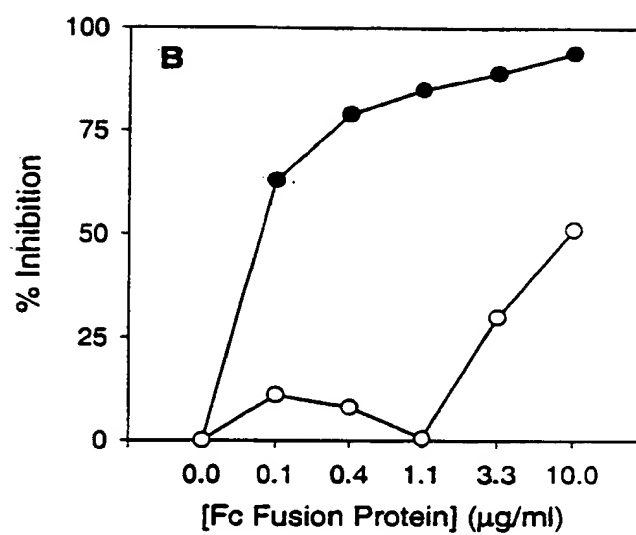
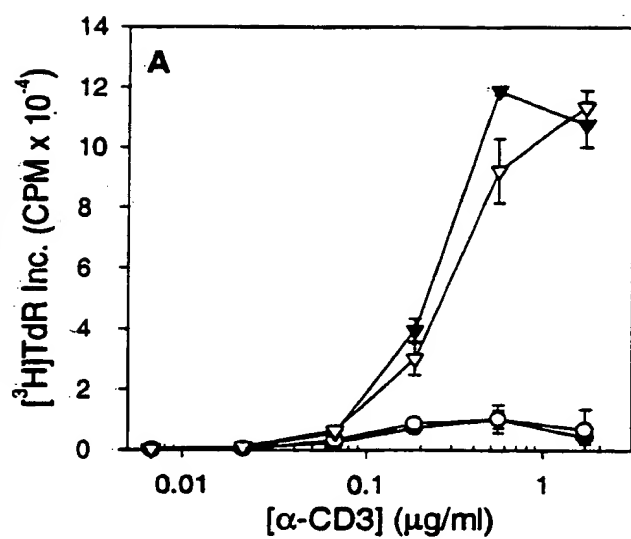


Figure 21C.

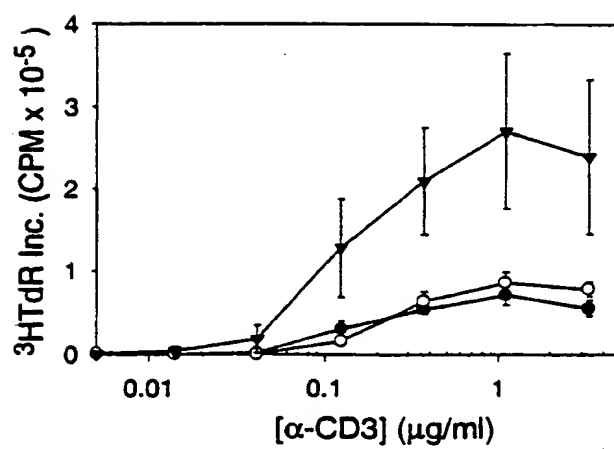


Figure 21D

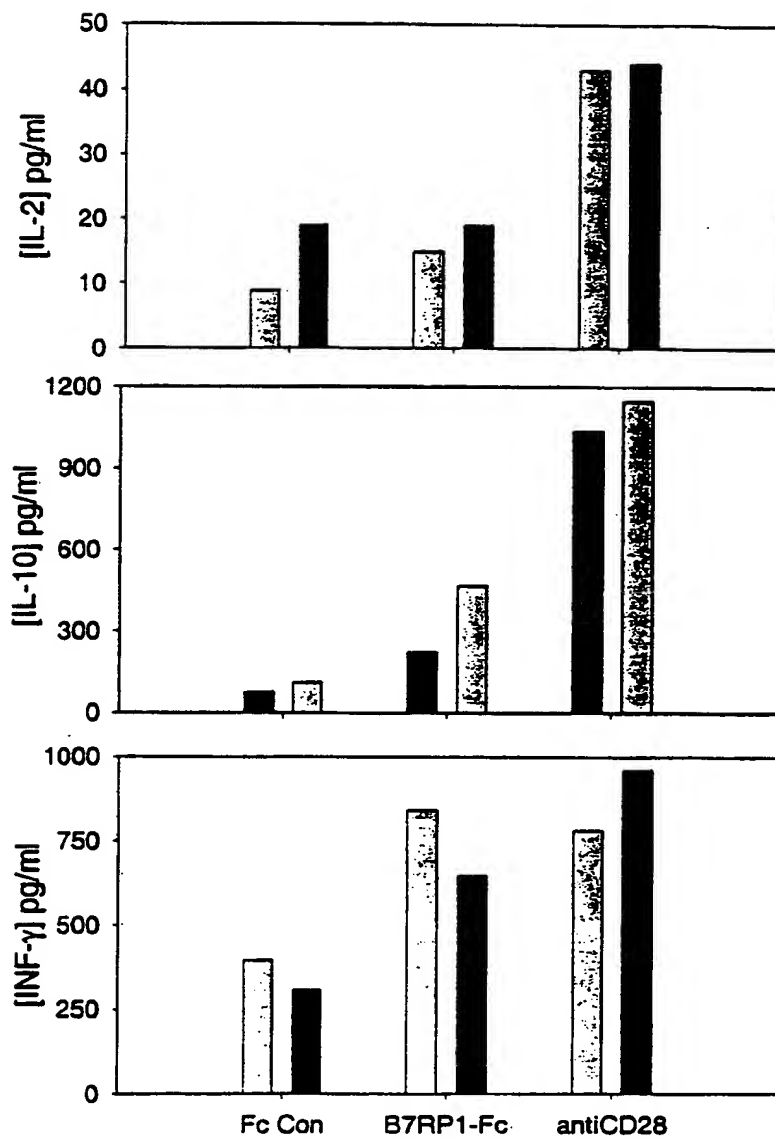
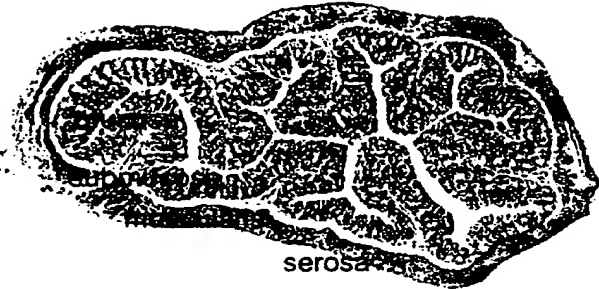


FIGURE 21D

PCT/US 00 '01871



A. Control mouse#53F:Prox. colon 40X



B. Mouse#111F:Prox. colon 40X



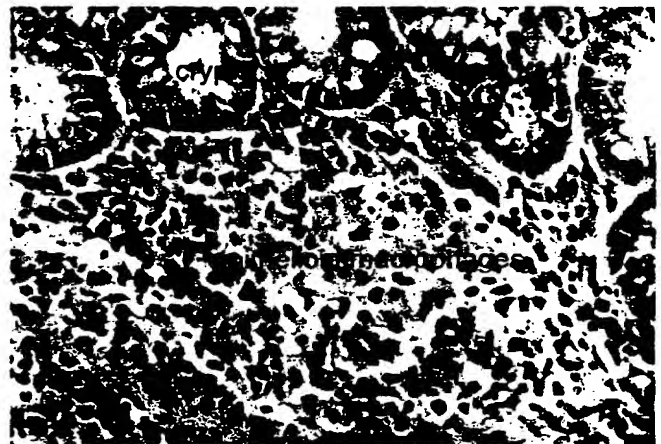
C. Mouse#111F: Prox. colon 20X



D. Mouse#111F: closeup of mucosa 100X



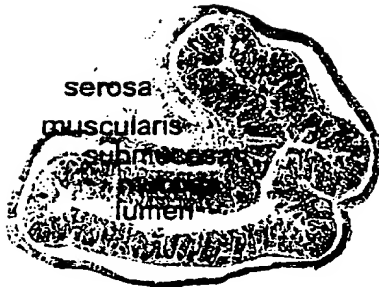
E. Mouse#112F: Giant cell, submucosa



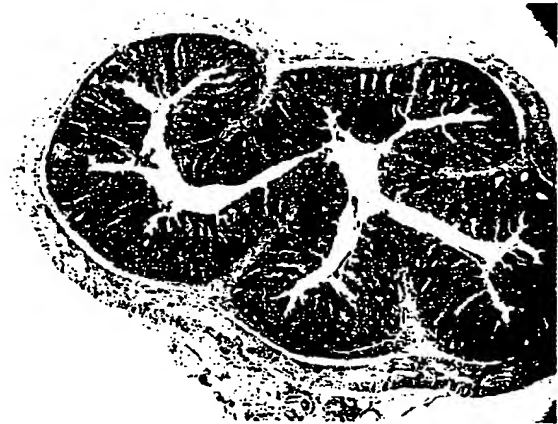
F. Mouse#112F:epithelioid macrophages

Figure 17

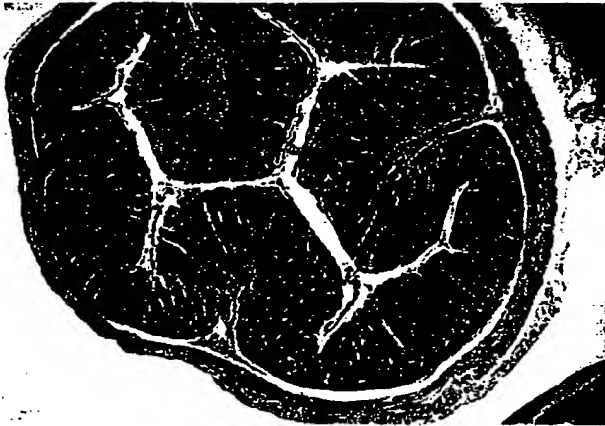
09890729-00000000



A. Control mouse#53F:Distal colon, 40X



B. mouse#111F:Distal colitis, 40X



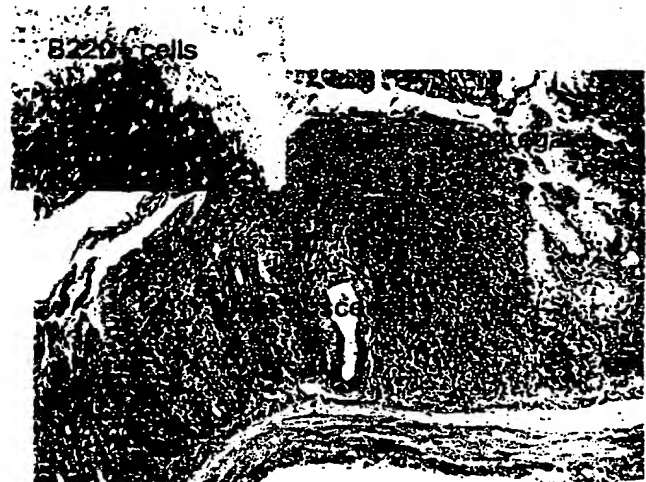
C. mouse#55M:Distal colitis, 40X



D. mouse#112F:Distal colon, 40X



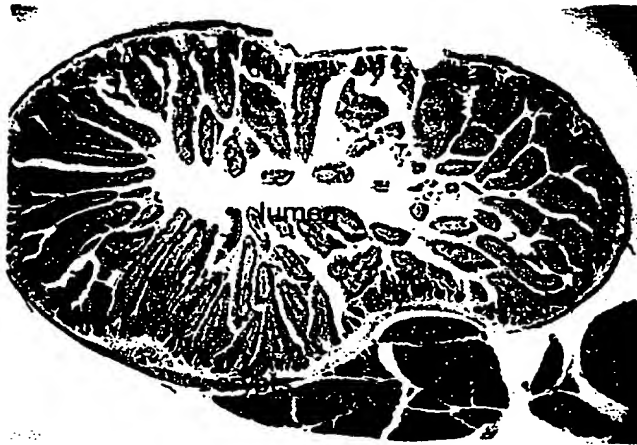
E. mouse#112:CD3+ T-cells, 40X



F. mouse#112:closeup, 100X

Figure 18

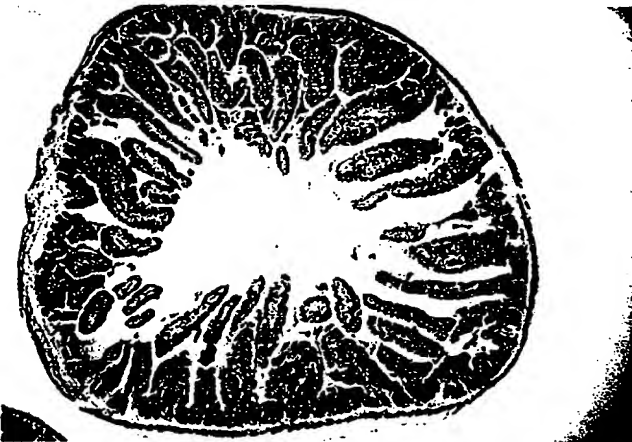
09/890729-000301



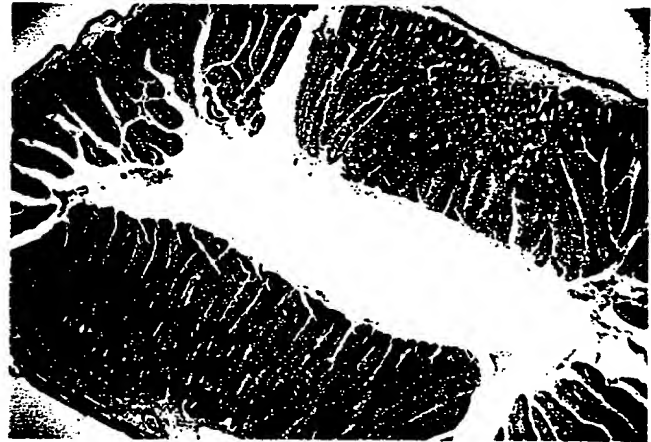
A. Control mouse#53F:duodenum, 40X



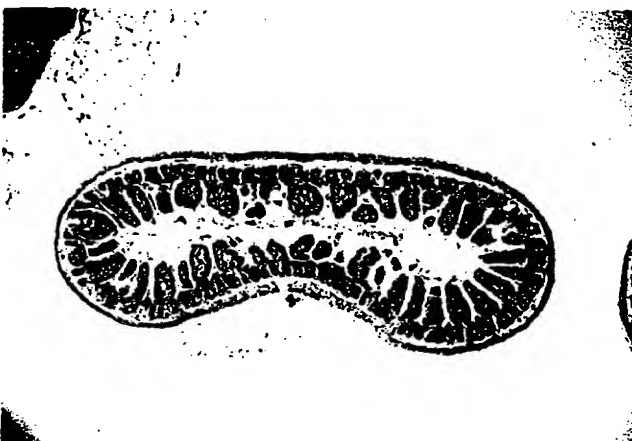
B. Mouse#51F:duodenum, 40X



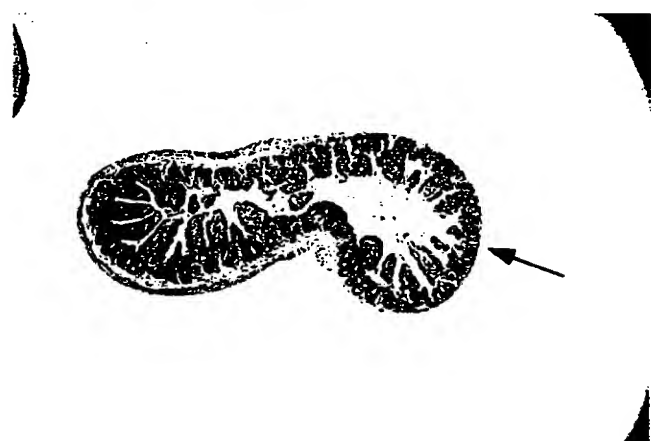
C. Control mouse#53F:jejunum, 40X



D. Mouse#51F:jejunal hyperplasia, 40X



E. Control mouse#53F:ileum, 40X



F. Mouse#231M:ileal atrophy, 40X

Figure 19